

SEQUENCE LISTING

<110> Fletcher, Jonathan A.
Kroll, Todd G.

<120> PAX8-PPARGgamma NUCLEIC ACID MOLECULES
AND POLYPEPTIDES AND USES THEREOF

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<150> US 60/177,109

<151> 2000-01-20

<150> US 60/225,079

<151> 2000-08-14

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Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp	
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Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys	
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Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu	
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aat aga atc atc cgg acc aaa gtg cag caa cca ttc aac ctc cct atg	432
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Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu	
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Ser	Gly	Val	Pro	Pro	Phe	Asn	Ala	Phe	Pro	His	Ala	Ala	Ser	Val	Tyr
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Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln
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cgc atc gta gac ctg gcc cac cag ggt gta agg ccc tgc gac atc tct     144
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser
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cgc cag ctc cgc gtc agc cat ggc tgc gtc agc aag atc ctt ggc agg     192
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg
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tac tac gag act ggc agc atc cgg cct gga gtg ata ggg ggc tcc aag     240
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys
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ccc aag gtg gcc acc ccc aag gtg gtg gag aag att ggg gac tac aaa     288
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys
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cgc cag aac cct acc atg ttt gcc tgg gag atc cga gac cgg ctc ctg     336
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu
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gct gag ggc gtc tgt gac aat gac act gtg ccc agt gtc agc tcc att     384
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile
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aat aga atc atc cgg acc aaa gtg cag caa cca ttc aac ctc cct atg     432
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met
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gac agc tgc gtg gcc acc aag tcc ctg agt ccc gga cac acg ctg atc     480
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile
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ccc agc tca gct gta act ccc ccg gag tca ccc cag tcg gat tcc ctg     528
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu
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ggc tcc acc tac tcc atc aat ggg ctc ctg ggc atc gct cag cct ggc     576
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly
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Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe	
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Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys	
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Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp	
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Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn	
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Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro His Ser Pro	
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Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly	
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Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Glu Met Thr Met	
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Val Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser	
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gac	att	cca	ttc	aca	aga	aca	gat	cca	gtg	gtt	gca	gat	tac	aag	tat	1392
Asp	Ile	Pro	Phe	Thr	Arg	Thr	Asp	Pro	Val	Val	Ala	Asp	Tyr	Lys	Tyr	
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Glu	Glu	Pro	Ser	Asn	Ser	Leu	Met	Ala	Ile	Glu	Cys	Arg	Val	Cys	Gly	
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Asp	Lys	Ala	Ser	Gly	Phe	His	Tyr	Gly	Val	His	Ala	Cys	Glu	Gly	Cys	
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Lys	Gly	Phe	Phe	Arg	Arg	Thr	Ile	Arg	Leu	Lys	Leu	Ile	Tyr	Asp	Arg	
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Cys	Asp	Leu	Asn	Cys	Arg	Ile	His	Lys	Lys	Ser	Arg	Asn	Lys	Cys	Gln	
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Tyr	Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	His	Asn	Ala	
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Ile	Arg	Phe	Gly	Arg	Met	Pro	Gln	Ala	Glu	Lys	Glu	Lys	Leu	Leu	Ala	
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Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Ser Lys	
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Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu	
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Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val	
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Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser	
740 745 750	
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Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala	
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Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe	
770 775 780	
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Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val	
785 790 795 800	
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Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu	
805 810 815	
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Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu	
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ctc cag aaa atg aca gac ctc aga cag att gtc acg gaa cac gtg cag	2544
Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln	
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cta ctg cag gtg atc aag aag acg gag aca gac atg agt ctt cac ccg	2592
Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro	
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2625

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Leu	Ser	Thr	His	Gln	Thr	Tyr	Pro	Val	Val	Ala	Asp	Pro	His	Ser	Pro
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Ser	Gly	Val	Pro	Phe	Asn	Ala	Phe	Pro	His	Ala	Ala	Ser	Val	Tyr	
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Val	Asp	Leu	Ser	Val	Met	Glu	Asp	His	Ser	His	Ser	Phe	Asp	Ile	Lys	
				420				425					430			
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Lys	Gly	Phe	Phe	Arg	Arg	Thr	Ile	Arg	Leu	Lys	Leu	Ile	Tyr	Asp	Arg	
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Cys	Asp	Leu	Asn	Cys	Arg	Ile	His	Lys	Lys	Ser	Arg	Asn	Lys	Cys	Gln	
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Tyr	Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	His	Asn	Ala	
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Ile	Arg	Phe	Gly	Arg	Met	Pro	Gln	Ala	Glu	Lys	Glu	Lys	Leu	Leu	Ala	
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Glu	Ile	Ser	Ser	Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	Ala	Asp	Leu	
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Asp	Lys	Ile	Lys	Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	Glu	Gln	Ser	Lys	
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Glu	Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	Arg	Ser	Val	Glu	
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Ala	Val	Gln	Glu	Ile	Thr	Glu	Tyr	Ala	Lys	Ser	Ile	Pro	Gly	Phe	Val	
	690					695					700					
Asn	Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	Tyr	Gly	Val	His	
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				805					810					815					
Gln	Leu	Lys	Leu	Asn	His	Pro	Glu	Ser	Ser	Gln	Leu	Phe	Ala	Lys	Leu				
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Leu	Gln	Lys	Met	Thr	Asp	Leu	Arg	Gln	Ile	Val	Thr	Glu	His	Val	Gln				
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      1              5              10

aac cag ctg gga ggg gcc ttt gtg aat ggc aga cct ctg ccg gaa gtg      97
Asn Gln Leu Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val
15              20              25

gtc cgc cag cgc atc gta gac ctg gcc cac cag ggt gta agg ccc tgc      145
Val Arg Gln Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys
30              35              40              45

gac atc tct cgc cag ctg cgc gtc agc cat ggt tgc gtc agc aag atc      193
Asp Ile Ser Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile
50              55              60

ctt ggc agg tac tac gag act ggc agc atc cgg cct gga gtg ata ggg      241
Leu Gly Arg Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly
65              70              75

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CCDS:CCDS1001.1

[illegible]

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Gly	Gly	Ala	Phe	Val	Asn	Gly	Arg	Pro	Leu	Pro	Glu	Val	Val	Arg	Gln
			20					25					30		
Arg	Ile	Val	Asp	Leu	Ala	His	Gln	Gly	Val	Arg	Pro	Cys	Asp	Ile	Ser
		35					40					45			
Arg	Gln	Leu	Arg	Val	Ser	His	Gly	Cys	Val	Ser	Lys	Ile	Leu	Gly	Arg
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<212> DNA
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			Met Gly	Glu Thr	Leu Gly Asp	
			1		5	
cct att gac	cca gaa agc	gat tcc ttc	act gat aca	ctg tct gca	aac	162
Ser						
ata tca caa	gaa atg acc	atg gtt gac	aca gag atg	cca ttc tgg	ccc	210
Pro Ile Asp	Pro Glu Ser	Asp Ser Phe	Thr Asp Thr	Leu Ser Ala	Asn	
10		15		20		
acc aac ttt	ggg atc agc	tcc gtg gat	ctc tcc gta	atg gaa gac	cac	258
Ile Ser Gln	Glu Met Thr	Met Val Asp	Thr Glu Met	Pro Phe Trp	Pro	
25		30		35	40	
tcc cac tcc	ttt gat atc	aag ccc ttc	act act gtt	gac ttc tcc	agc	306
Thr Asn Phe	Gly Ile Ser	Ser Val Asp	Leu Ser Val	Met Glu Asp	His	
	45		50		55	
att tct act	cca cat tac	gaa gac att	cca ttc aca	aga aca gat	cca	354
Ser His Ser	Phe Asp Ile	Lys Pro Phe	Thr Thr Val	Asp Phe Ser	Ser	
	60		65		70	
gtg gtt gca	gat tac aag	tat gac ctg	aaa ctt caa	gag tac caa	agt	402
Ile Ser Thr	Pro His Tyr	Glu Asp Ile	Pro Phe Thr	Arg Thr Asp	Pro	
75		80		85		
gca atc aaa	gtg gag cct	gca tct cca	cct tat tat	tct gag aag	act	450
Val Val Ala	Asp Tyr Lys	Tyr Asp Leu	Lys Leu Gln	Glu Tyr Gln	Ser	
90		95		100		
cag ctc tac	aat aag cct	cat gaa gag	cct tcc aac	tcc ctc atg	gca	498
Ala Ile Lys	Val Glu Pro	Ala Ser Pro	Pro Tyr Tyr	Ser Glu Lys	Thr	
105		110		115	120	
att gaa tgt	cgt gtc tgt	gga gat aaa	gct tct gga	ttt cac tat	gga	546
Gln Leu Tyr	Asn Lys Pro	His Glu Glu	Pro Ser Asn	Ser Leu Met	Ala	
	125		130		135	
gtt cat gct	tgt gaa gga	tgc aag ggt	ttc ttc cgg	aga aca atc	aga	594
Ile Glu Cys	Arg Val Cys	Gly Asp Lys	Ala Ser Gly	Phe His Tyr	Gly	
	140		145		150	
ttg aag ctt	atc tat gac	aga tgt gat	ctt aac tgt	cgg atc cac	aaa	642
Val His Ala	Cys Glu Gly	Cys Lys Gly	Phe Phe Arg	Thr Ile Arg		
155		160		165		
aaa agt aga	aat aaa tgt	cag tac tgt	cgg ttt cag	aaa tgc ctt	gca	690
Leu Lys Leu	Ile Tyr Asp	Arg Cys Asp	Leu Asn Cys	Arg Ile His	Lys	
170		175		180		

096511-011304

gtg ggg atg tct cat aat gcc atc agg ttt ggg cgg atg cca cag gcc	738
Lys Ser Arg Asn Lys Cys Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala	
185 190 195 200	
gag aag gag aag ctg ttg gcg gag atc tcc agt gat atc gac cag ctg	786
Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met Pro Gln Ala	
205 210 215	
aat cca gag tcc gct gac ctc cgg gcc ctg gca aaa cat ttg tat gac	834
Glu Lys Glu Lys Leu Leu Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu	
220 225 230	
tca tac ata aag tcc ttc ccg ctg acc aaa gca aag gcg agg gcg atc	882
Asn Pro Glu Ser Ala Asp Leu Arg Ala Leu Ala Lys His Leu Tyr Asp	
235 240 245	
ttg aca gga aag aca aca gac aaa tca cca ttc gtt atc tat gac atg	930
Ser Tyr Ile Lys Ser Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile	
250 255 260	
aat tcc tta atg atg gga gaa gat aaa atc aag ttc aaa cac atc acc	978
Leu Thr Gly Lys Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met	
265 270 275 280	
ccc ctg cag gag cag agc aaa gag gtg gcc atc cgc atc ttt cag ggc	1026
Asn Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr	
285 290 295	
tgc cag ttt cgc tcc gtg gag gct gtg cag gag atc aca gag tat gcc	1074
Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly	
300 305 310	
aaa agc att cct ggt ttt gta aat ctt gac ttg aac gac caa gta act	1122
Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala	
315 320 325	
ctc ctc aaa tat gga gtc cac gag atc att tac aca atg ctg gcc tcc	1170
Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr	
330 335 340	
ttg atg aat aaa gat ggg gtt ctc ata tcc gag ggc caa ggc ttc atg	1218
Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser	
345 350 355 360	
aca agg gag ttt cta aag agc ctg cga aag cct ttt ggt gac ttt atg	1266
Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met	
365 370 375	
gag ccc aag ttt gag ttt gct gtg aag ttc aat gca ctg gaa tta gat	1314
Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met	
380 385 390	
gac agc gac ttg gca ata ttt att gct gtc att att ctc agt gga gac	1362
Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp	
395 400 405	

09765441011301

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Phe	Thr	Asp	Thr	Leu	Ser	Ala	Asn	Ile	Ser	Gln	Glu	Met	Thr	Met	Val
			20					25					30		
Asp	Thr	Glu	Met	Pro	Phe	Trp	Pro	Thr	Asn	Phe	Gly	Ile	Ser	Ser	Val
		35					40					45			
Asp	Leu	Ser	Val	Met	Glu	Asp	His	Ser	His	Ser	Phe	Asp	Ile	Lys	Pro
	50					55					60				
Phe 65	Thr	Thr	Val	Asp	Phe	Ser	Ser	Ile	Ser	Thr	Pro	His	Tyr	Glu	Asp
				70						75				80	
Ile	Pro	Phe	Thr	Arg	Thr	Asp	Pro	Val	Val	Ala	Asp	Tyr	Lys	Tyr	Asp
				85					90				95		
Leu	Lys	Leu	Gln	Glu	Tyr	Gln	Ser	Ala	Ile	Lys	Val	Glu	Pro	Ala	Ser
			100					105					110		
Pro	Pro	Tyr	Tyr	Ser	Glu	Lys	Thr	Gln	Leu	Tyr	Asn	Lys	Pro	His	Glu
		115					120					125			
Glu	Pro	Ser	Asn	Ser	Leu	Met	Ala	Ile	Glu	Cys	Arg	Val	Cys	Gly	Asp
	130					135					140				
Lys 145	Ala	Ser	Gly	Phe	His	Tyr	Gly	Val	His	Ala	Cys	Glu	Gly	Cys	Lys
				150						155				160	
Gly	Phe	Phe	Arg	Arg	Thr	Ile	Arg	Leu	Lys	Leu	Ile	Tyr	Asp	Arg	Cys
			165						170				175		
Asp	Leu	Asn	Cys	Arg	Ile	His	Lys	Lys	Ser	Arg	Asn	Lys	Cys	Gln	Tyr
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21

18

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<210> 22
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agccccgagc cctcggcggg ctgcgagcga ctccccggcg atg cct cac aac tcc          175
                                         Met Pro His Asn
                                         1

atc aga tct ggc cat gga ggg ctg aac cag ctg gga ggg gcc ttt gtg          223
Ser
5

aat ggc aga cct ctg ccg gaa gtg gtc cgc cag cgc atc gta gac ctg          271
Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu Gly Gly Ala Phe Val
                        10                        15                        20

gcc cac cag ggt gta agg ccc tgc gac atc tct cgc cag ctc cgc gtc          319
Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln Arg Ile Val Asp Leu
                        25                        30                        35

agc cat ggc tgc gtc agc aag atc ctt ggc agg tac tac gag act ggc          367
Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser Arg Gln Leu Arg Val
                        40                        45                        50

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agc	atc	cgg	cct	gga	gtg	ata	ggg	ggc	tcc	aag	ccc	aag	gtg	gcc	acc	415
Ser	His	Gly	Cys	Val	Ser	Lys	Ile	Leu	Gly	Arg	Tyr	Tyr	Glu	Thr	Gly	
	55					60					65					
ccc	aag	gtg	gtg	gag	aag	att	ggg	gac	tac	aaa	cgc	cag	aac	cct	acc	463
Ser	Ile	Arg	Pro	Gly	Val	Ile	Gly	Gly	Ser	Lys	Pro	Lys	Val	Ala	Thr	
	70				75					80					85	
atg	ttt	gcc	tgg	gag	atc	cga	gac	cgg	ctc	ctg	gct	gag	ggc	gtc	tgt	511
Pro	Lys	Val	Val	Glu	Lys	Ile	Gly	Asp	Tyr	Lys	Arg	Gln	Asn	Pro	Thr	
				90					95					100		
gac	aat	gac	act	gtg	ccc	agt	gtc	agc	tcc	att	aat	aga	atc	atc	cgg	559
Met	Phe	Ala	Trp	Glu	Ile	Arg	Asp	Arg	Leu	Leu	Ala	Glu	Gly	Val	Cys	
			105					110					115			
acc	aaa	gtg	cag	caa	cca	ttc	aac	ctc	cct	atg	gac	agc	tgc	gtg	gcc	607
Asp	Asn	Asp	Thr	Val	Pro	Ser	Val	Ser	Ser	Ile	Asn	Arg	Ile	Ile	Arg	
		120				125						130				
acc	aag	tcc	ctg	agt	ccc	gga	cac	acg	ctg	atc	ccc	agc	tca	gct	gta	655
Thr	Lys	Val	Gln	Gln	Pro	Phe	Asn	Leu	Pro	Met	Asp	Ser	Cys	Val	Ala	
	135					140					145					
act	ccc	ccg	gag	tca	ccc	cag	tcg	gat	tcc	ctg	ggc	tcc	acc	tac	tcc	703
Thr	Lys	Ser	Leu	Ser	Pro	Gly	His	Thr	Leu	Ile	Pro	Ser	Ser	Ala	Val	
	150				155					160					165	
atc	aat	ggg	ctc	ctg	ggc	atc	gct	cag	cct	ggc	agc	gac	aag	agg	aaa	751
Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	Asp	Ser	Leu	Gly	Ser	Thr	Tyr	Ser	
				170					175					180		
atg	gat	gac	agt	gat	cag	gat	agc	tgc	cga	cta	agc	att	gac	tca	cag	799
Ile	Asn	Gly	Leu	Leu	Gly	Ile	Ala	Gln	Pro	Gly	Ser	Asp	Lys	Arg	Lys	
			185					190					195			
agc	agc	agc	agc	gga	ccc	cga	aag	cac	ctt	cgc	acg	gat	gcc	ttc	agc	847
Met	Asp	Asp	Ser	Asp	Gln	Asp	Ser	Cys	Arg	Leu	Ser	Ile	Asp	Ser	Gln	
		200				205						210				
cag	cac	cac	ctc	gag	ccg	ctc	gag	tgc	cca	ttt	gag	cgg	cag	cac	tac	895
Ser	Ser	Ser	Ser	Gly	Pro	Arg	Lys	His	Leu	Arg	Thr	Asp	Ala	Phe	Ser	
	215					220					225					
cca	gag	gcc	tat	gcc	tcc	ccc	agc	cac	acc	aaa	ggc	gag	cag	ggc	ctc	943
Gln	His	His	Leu	Glu	Pro	Leu	Glu	Cys	Pro	Phe	Glu	Arg	Gln	His	Tyr	
	230				235					240					245	
tac	ccg	ctg	ccc	ttg	ctc	aac	agc	acc	ctg	gac	gac	ggg	aag	gcc	acc	991
Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys	Gly	Glu	Gln	Gly	Leu	
				250					255					260		
ctg	acc	cct	tcc	aac	acg	cca	ctg	ggg	cgc	aac	ctc	tcg	act	cac	cag	

acc tac ccc gtg gtg gca ggg cga gag atg gtg ggg ccc acg ctg ccc	1087
Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn Leu Ser Thr His Gln	
280 285 290	
gga tac cca ccc cac atc ccc acc agc gga cag ggc agc tat gcc tcc	1135
Thr Tyr Pro Val Val Ala Gly Arg Glu Met Val Gly Pro Thr Leu Pro	
295 300 305	
tct gcc atc gca ggc atg gtg gca gaa atg acc atg gtt gac aca gag	1183
Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly Ser Tyr Ala Ser	
310 315 320 325	
atg cca ttc tgg ccc acc aac ttt ggg atc agc tcc gtg gat ctc tcc	1231
Ser Ala Ile Ala Gly Met Val Ala Glu Met Thr Met Val Asp Thr Glu	
330 335 340	
gta atg gaa gac cac tcc cac tcc ttt gat atc aag ccc ttc act act	1279
Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val Asp Leu Ser	
345 350 355	
gtt gac ttc tcc agc att tct act cca cat tac gaa gac att cca ttc	1327
Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro Phe Thr Thr	
360 365 370	
aca aga aca gat cca gtg gtt gca gat tac aag tat gac ctg aaa ctt	1375
Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp Ile Pro Phe	
375 380 385	
caa gag tac caa agt gca atc aaa gtg gag cct gca tct cca cct tat	1423
Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp Leu Lys Leu	
390 395 400 405	
tat tct gag aag act cag ctc tac aat aag cct cat gaa gag cct tcc	1471
Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser Pro Pro Tyr	
410 415 420	
aac tcc ctc atg gca att gaa tgt cgt gtc tgt gga gat aaa gct tct	1519
Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu Glu Pro Ser	
425 430 435	
gga ttt cac tat gga gtt cat gct tgt gaa gga tgc aag ggt ttc ttc	1567
Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp Lys Ala Ser	
440 445 450	
cgg aga aca atc aga ttg aag ctt atc tat gac aga tgt gat ctt aac	1615
Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe	
455 460 465	
tgt cgg atc cac aaa aaa agt aga aat aaa tgt cag tac tgt cgg ttt	1663
Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys Asp Leu Asn	
470 475 480 485	
cag aaa tgc ctt gca gtg ggg atg tct cat aat gcc atc agg ttt ggg	1711
Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr Cys Arg Phe	
490 495 500	

cgg atg cca cag gcc gag aag gag aag ctg ttg gcg gag atc tcc agt	1759
Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile Arg Phe Gly	
505 510 515	
gat atc gac cag ctg aat cca gag tcc gct gac ctc cgg gcc ctg gca	1807
Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu Ile Ser Ser	
520 525 530	
aaa cat ttg tat gac tca tac ata aag tcc ttc ccg ctg acc aaa gca	1855
Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg Ala Leu Ala	
535 540 545	
aag gcg agg gcg atc ttg aca gga aag aca aca gac aaa tca cca ttc	1903
Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu Thr Lys Ala	
550 555 560 565	
gtt atc tat gac atg aat tcc tta atg atg gga gaa gat aaa atc aag	1951
Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys Ser Pro Phe	
570 575 580	
ttc aaa cac atc acc ccc ctg cag gag cag agc aaa gag gtg gcc atc	1999
Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp Lys Ile Lys	
585 590 595	
cgc atc ttt cag ggc tgc cag ttt cgc tcc gtg gag gct gtg cag gag	2047
Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile	
600 605 610	
atc aca gag tat gcc aaa agc att cct ggt ttt gta aat ctt gac ttg	2095
Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu	
615 620 625	
aac gac caa gta act ctc ctc aaa tat gga gtc cac gag atc att tac	2143
Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu	
630 635 640 645	
aca atg ctg gcc tcc ttg atg aat aaa gat ggg gtt ctc ata tcc gag	2191
Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr	
650 655 660	
ggc caa ggc ttc atg aca agg gag ttt cta aag agc ctg cga aag cct	2239
Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu	
665 670 675	
ttt ggt gac ttt atg gag ccc aag ttt gag ttt gct gtg aag ttc aat	2287
Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro	
680 685 690	
gca ctg gaa tta gat gac agc gac ttg gca ata ttt att gct gtc att	2335
Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn	
695 700 705	
att ctc agt gga gac cgc cca ggt ttg ctg aat gtg aag ccc att gaa	2383
Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala Val Ile	
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<212> PRT
<213> Homo Sapiens

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Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser
35          40          45
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg
50          55          60
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys
65          70          75          80
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys
85          90          95
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu
100         105         110
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile
115         120         125
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met
130         135         140
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile
145         150         155         160
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu
165         170         175
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly
180         185         190
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu
195         200         205
Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg
210         215         220

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Thr	Asp	Ala	Phe	Ser	Gln	His	His	Leu	Glu	Pro	Leu	Glu	Cys	Pro	Phe
225					230					235					240
Glu	Arg	Gln	His	Tyr	Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys
				245					250						255
Gly	Glu	Gln	Gly	Leu	Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp
			260					265					270		
Asp	Gly	Lys	Ala	Thr	Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	Gly	Arg	Asn
		275					280					285			
Leu	Ser	Thr	His	Gln	Thr	Tyr	Pro	Val	Val	Ala	Gly	Arg	Glu	Met	Val
	290					295					300				
Gly	Pro	Thr	Leu	Pro	Gly	Tyr	Pro	Pro	His	Ile	Pro	Thr	Ser	Gly	Gln
305					310					315					320
Gly	Ser	Tyr	Ala	Ser	Ser	Ala	Ile	Ala	Gly	Met	Val	Ala	Glu	Met	Thr
				325					330						335
Met	Val	Asp	Thr	Glu	Met	Pro	Phe	Trp	Pro	Thr	Asn	Phe	Gly	Ile	Ser
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Ser	Val	Asp	Leu	Ser	Val	Met	Glu	Asp	His	Ser	His	Ser	Phe	Asp	Ile
		355					360						365		
Lys	Pro	Phe	Thr	Thr	Val	Asp	Phe	Ser	Ser	Ile	Ser	Thr	Pro	His	Tyr
	370					375						380			
Glu	Asp	Ile	Pro	Phe	Thr	Arg	Thr	Asp	Pro	Val	Val	Ala	Asp	Tyr	Lys
385						390					395				400
Tyr	Asp	Leu	Lys	Leu	Gln	Glu	Tyr	Gln	Ser	Ala	Ile	Lys	Val	Glu	Pro
				405					410					415	
Ala	Ser	Pro	Pro	Tyr	Tyr	Ser	Glu	Lys	Thr	Gln	Leu	Tyr	Asn	Lys	Pro
			420					425						430	
His	Glu	Glu	Pro	Ser	Asn	Ser	Leu	Met	Ala	Ile	Glu	Cys	Arg	Val	Cys
			435				440						445		
Gly	Asp	Lys	Ala	Ser	Gly	Phe	His	Tyr	Gly	Val	His	Ala	Cys	Glu	Gly
	450					455					460				
Cys	Lys	Gly	Phe	Phe	Arg	Arg	Thr	Ile	Arg	Leu	Lys	Leu	Ile	Tyr	Asp
465					470					475					480
Arg	Cys	Asp	Leu	Asn	Cys	Arg	Ile	His	Lys	Lys	Ser	Arg	Asn	Lys	Cys
				485					490					495	
Gln	Tyr	Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	His	Asn
			500					505						510	
Ala	Ile	Arg	Phe	Gly	Arg	Met	Pro	Gln	Ala	Glu	Lys	Glu	Lys	Leu	Leu
	515						520						525		
Ala	Glu	Ile	Ser	Ser	Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	Ala	Asp
	530					535					540				
Leu	Arg	Ala	Leu	Ala	Lys	His	Leu	Tyr	Asp	Ser	Tyr	Ile	Lys	Ser	Phe
545					550					555					560
Pro	Leu	Thr	Lys	Ala	Lys	Ala	Arg	Ala	Ile	Leu	Thr	Gly	Lys	Thr	Thr
				565					570					575	
Asp	Lys	Ser	Pro	Phe	Val	Ile	Tyr	Asp	Met	Asn	Ser	Leu	Met	Met	Gly
			580					585					590		
Glu	Asp	Lys	Ile	Lys	Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	Glu	Gln	Ser
		595					600						605		
Lys	Glu	Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	Arg	Ser	Val
	610					615						620			
Glu	Ala	Val	Gln	Glu	Ile	Thr	Glu	Tyr	Ala	Lys	Ser	Ile	Pro	Gly	Phe
625					630					635					640
Val	Asn	Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	Tyr	Gly	Val
				645					650					655	
His	Glu	Ile	Ile	Tyr	Thr	Met	Leu	Ala	Ser	Leu	Met	Asn	Lys	Asp	Gly
			660					665						670	

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Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys
675 680 685
Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe
690 695 700
Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile
705 710 715 720
Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn
725 730 735
Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu
740 745 750
Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys
755 760 765
Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val
770 775 780
Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His
785 790 795 800
Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
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agccccgagc cctcggcggg ctgcgagcga ctccccggcg atg cct cac aac tcc 175
Met Pro His Asn Ser
1 5
atc aga tct ggc cat gga ggg ctg aac cag ctg gga ggg gcc ttt gtg 223
Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu Gly Gly Ala Phe Val
10 15 20
aat ggc aga cct ctg ccg gaa gtg gtc cgc cag cgc atc gta gac ctg 271
Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln Arg Ile Val Asp Leu
25 30 35
gcc cac cag ggt gta agg ccc tgc gac atc tct cgc cag ctc cgc gtc 319
Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser Arg Gln Leu Arg Val
40 45 50
agc cat ggc tgc gtc agc aag atc ctt ggc agg tac tac gag act ggc 367
Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg Tyr Tyr Glu Thr Gly
55 60 65
agc atc cgg cct gga gtg ata ggg ggc tcc aag ccc aag gtg gcc acc 415
Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys Pro Lys Val Ala Thr
70 75 80 85
ccc aag gtg gtg gag aag att ggg gac tac aaa cgc cag aac cct acc 463

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Pro	Lys	Val	Val	Glu	Lys	Ile	Gly	Asp	Tyr	Lys	Arg	Gln	Asn	Pro	Thr	
				90					95					100		
atg	ttt	gcc	tgg	gag	atc	cga	gac	cgg	ctc	ctg	gct	gag	ggc	gtc	tgt	511
Met	Phe	Ala	Trp	Glu	Ile	Arg	Asp	Arg	Leu	Leu	Ala	Glu	Gly	Val	Cys	
			105					110					115			
gac	aat	gac	act	gtg	ccc	agt	gtc	agc	tcc	att	aat	aga	atc	atc	cgg	559
Asp	Asn	Asp	Thr	Val	Pro	Ser	Val	Ser	Ser	Ile	Asn	Arg	Ile	Ile	Arg	
			120					125				130				
acc	aaa	gtg	cag	caa	cca	ttc	aac	ctc	cct	atg	gac	agc	tgc	gtg	gcc	607
Thr	Lys	Val	Gln	Gln	Pro	Phe	Asn	Leu	Pro	Met	Asp	Ser	Cys	Val	Ala	
			135				140					145				
acc	aag	tcc	ctg	agt	ccc	gga	cac	acg	ctg	atc	ccc	agc	tca	gct	gta	655
Thr	Lys	Ser	Leu	Ser	Pro	Gly	His	Thr	Leu	Ile	Pro	Ser	Ser	Ala	Val	
			150			155				160					165	
act	ccc	ccg	gag	tca	ccc	cag	tcg	gat	tcc	ctg	ggc	tcc	acc	tac	tcc	703
Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	Asp	Ser	Leu	Gly	Ser	Thr	Tyr	Ser	
				170					175					180		
atc	aat	ggg	ctc	ctg	ggc	atc	gct	cag	cct	ggc	agc	gac	aag	agg	aaa	751
Ile	Asn	Gly	Leu	Leu	Gly	Ile	Ala	Gln	Pro	Gly	Ser	Asp	Lys	Arg	Lys	
			185					190					195			
atg	gat	gac	agt	gat	cag	gat	agc	tgc	cga	cta	agc	att	gac	tca	cag	799
Met	Asp	Asp	Ser	Asp	Gln	Asp	Ser	Cys	Arg	Leu	Ser	Ile	Asp	Ser	Gln	
			200				205					210				
agc	agc	agc	agc	gga	ccc	cga	aag	cac	ctt	cgc	acg	gat	gcc	ttc	agc	847
Ser	Ser	Ser	Ser	Gly	Pro	Arg	Lys	His	Leu	Arg	Thr	Asp	Ala	Phe	Ser	
			215				220				225					
cag	cac	cac	ctc	gag	ccg	ctc	gag	tgc	cca	ttt	gag	cgg	cag	cac	tac	895
Gln	His	His	Leu	Glu	Pro	Leu	Glu	Cys	Pro	Phe	Glu	Arg	Gln	His	Tyr	
			230			235				240					245	
cca	gag	gcc	tat	gcc	tcc	ccc	agc	cac	acc	aaa	ggc	gag	cag	ggc	ctc	943
Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys	Gly	Glu	Gln	Gly	Leu	
				250					255					260		
tac	ccg	ctg	ccc	ttg	ctc	aac	agc	acc	ctg	gac	gac	ggg	aag	gcc	acc	991
Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp	Asp	Gly	Lys	Ala	Thr	
			265					270					275			
ctg	acc	cct	tcc	aac	acg	cca	ctg	ggg	cgc	aac	ctc	tcg	act	cac	cag	1039
Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	Gly	Arg	Asn	Leu	Ser	Thr	His	Gln	
			280				285					290				
acc	tac	ccc	gtg	gtg	gca	gat	cct									

Glu Thr Pro Glu Val Ser Ser Ser Ser Ser Thr Pro Cys Ser Leu Ser	
310 315 320 325	
agc tcc gcc ctt ttg gat ctg cag caa gtc ggc tcc ggg gtc ccg ccc	1183
Ser Ser Ala Leu Leu Asp Leu Gln Gln Val Gly Ser Gly Val Pro Pro	
330 335 340	
ttc aat gcc ttt ccc cat gct gcc tcc gtg tac ggg cag ttc acg ggc	1231
Phe Asn Ala Phe Pro His Ala Ala Ser Val Tyr Gly Gln Phe Thr Gly	
345 350 355	
cag gcc ctc ctc tca ggg cga gag atg gtg ggg ccc acg ctg ccc gga	1279
Gln Ala Leu Leu Ser Gly Arg Glu Met Val Gly Pro Thr Leu Pro Gly	
360 365 370	
tac cca ccc cac atc ccc acc agc gga cag ggc agc tat gcc tcc tct	1327
Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly Ser Tyr Ala Ser Ser	
375 380 385	
gcc atc gca ggc atg gtg gca gga agt gaa tac tct ggc aat gcc tat	1375
Ala Ile Ala Gly Met Val Ala Gly Ser Glu Tyr Ser Gly Asn Ala Tyr	
390 395 400 405	
ggc cac acc ccc tac tcc tcc tac agc gag gcc tgg ggc ttc ccc aac	1423
Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu Ala Trp Gly Phe Pro Asn	
410 415 420	
tcc agc ttg ctg agt tcc cca tat tat tac agt tcc aca tca agg ccg	1471
Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Tyr Ser Ser Thr Ser Arg Pro	
425 430 435	
agt gca ccg ccc acc act gcc acg gcc ttt gac cat ctg tagttgccat	1520
Ser Ala Pro Pro Thr Thr Ala Thr Ala Phe Asp His Leu	
440 445 450	
ggggacagtg ggagcgcactg agcaacagga ggactcagcc tgggacaggc cccagagagt	1580
cacacaaaagg aatcttttatt attacatgaa aaataaccac aagtccagca ttgcggcaca	1640
ctccctgtgt ggttaatttta atgaacctg aaagacagga tgaccttgga caaggccaaa	1700
ctgtctctca agactcctta atgaggggca ggagtcccag ggaaagagaa ccatgccatg	1760
ctgaaaaaga caaaattgaa gaagaaatgt agccccagcc ggtacctcc aaaggagaga	1820
agaagcaata gccgaggaac ttggggggat ggcgaaatggt tcctgcccgg gcccaaggg	1880
gcacagggca cctccatggc tccattatta acacaactct agcaattatg gaccataagc	1940
acttccctcc agcccacaag tcacagcctg gtgcccaggc tctgctcacc agccaccag	2000
ggagtcacct cctcagcct cccgcctgcc ccacacggag gctctggctg tcctctttcc	2060
tccactccat ttgcttggct ctttctacac ctccctcttg gatgggctga gggctggagc	2120
gagtccttca gaaattccac caggctgtca gctgacctct ttttctgct gctgtgaagg	2180
tatagcacca cccaggtcct cctgcagtgc ggcaccccct tggcagctgc cgtcagccag	2240
gccagcccca gggagcttaa aacagacatt ccacagggcc tgggcccctg ggaggtgagg	2300
tgtggtgtgc ggcttcaccc agggcagaac aaggcagaat cgcaggaaac ccgcttcccc	2360
ttcctgacag ctccctgcca gccaaatgtg cttcctgcag ctacgcccc ccagctactg	2420
aagggaacca aggcaccccc tgaagccagc gatagagggc ccctctctgc tccccagcag	2480
ctcctgcccc caaggcctga ctgtatatac tgtaaataaa actttgtttg ggtcaagctt	2540
ccttctttct aacccccaga ctttggcctc tgagtgaat gtctctctt gccctgtggg	2600
gcttctctcc ttgatgcttc tttctttttt taaagacaac ctgccattac cacatgactc	2660
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 <213> Homo Sapiens

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 20 25 30
 Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser
 35 40 45
 Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg
 50 55 60
 Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys
 65 70 75 80
 Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys
 85 90 95
 Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu
 100 105 110
 Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile
 115 120 125
 Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met
 130 135 140
 Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile
 145 150 155 160
 Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu
 165 170 175
 Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly
 180 185 190
 Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu
 195 200 205
 Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg
 210 215 220
 Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe
 225 230 235 240
 Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys
 245 250 255
 Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp
 260 265 270
 Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn
 275 280 285
 Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro His Ser Pro
 290 295 300
 Leu Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser Ser Ser Thr
 305 310 315 320
 Pro Cys Ser Leu Ser Ser Ser Ala Leu Leu Asp Leu Gln Gln Val Gly
 325 330 335
 Ser Gly Val Pro Pro Phe Asn Ala Phe Pro His Ala Ala Ser Val Tyr
 340 345 350
 Gly Gln Phe Thr Gly Gln Ala Leu Ser Gly Arg Glu Met Val Gly
 355 360 365
 Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly
 370 375 380
 Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Gly Ser Glu Tyr
 385 390 395 400

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Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu Ala
405 410 415
Trp Gly Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Tyr Ser
420 425 430
Ser Thr Ser Arg Pro Ser Ala Pro Pro Thr Thr Ala Thr Ala Phe Asp
435 440 445
His Leu
450

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<212> DNA
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ggtcggcctc gaggacaccg gagaggggcg ccacgccgcc gtggccgcag aa atg acc 178
Met Thr
1

atg gtt gac aca gag atc gca ttc tgg ccc acc aac ttt ggg atc agc 226
Met Val Asp Thr Glu Ile Ala Phe Trp Pro Thr Asn Phe Gly Ile Ser
5 10 15

tcc gtg gat ctc tcc gta atg gaa gac cac tcc cac tcc ttt gat atc 274
Ser Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile
20 25 30

aag ccc ttc act act gtt gac ttc tcc agc att tct act cca cat tac 322
Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr
35 40 45 50

gaa gac att cca ttc aca aga aca gat cca gtg gtt gca gat tac aag 370
Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys
55 60 65

tat gac ctg aaa ctt caa gag tac caa agt gca atc aaa gtg gag cct 418
Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro
70 75 80

gca tct cca cct tat tat tct gag aag act cag ctc tac aat aag cct 466
Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro
85 90 95

cat gaa gag cct tcc aac tcc ctc atg gca att gaa tgt cgt gtc tgt 514
His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys
100 105 110

gga gat aaa gct tct gga ttt cac tat gga gtt cat gct tgt gaa gga 562
Gly Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly
115 120 125 130

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tgc	aag	ggt	ttc	ttc	cgg	aga	aca	atc	aga	ttg	aag	ctt	atc	tat	gac		610
Cys	Lys	Gly	Phe	Phe	Arg	Arg	Thr	Ile	Arg	Leu	Lys	Leu	Ile	Tyr	Asp		
				135						140					145		
aga	tgt	gat	ctt	aac	tgt	cgg	atc	cac	aaa	aaa	agt	aga	aat	aaa	tgt		658
Arg	Cys	Asp	Leu	Asn	Cys	Arg	Ile	His	Lys	Lys	Ser	Arg	Asn	Lys	Cys		
			150					155						160			
cag	tac	tgt	cgg	ttt	cag	aaa	tgc	ctt	gca	gtg	ggg	atg	tct	cat	aat		706
Gln	Tyr	Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	His	Asn		
		165					170						175				
gcc	atc	agg	ttt	ggg	cgg	atc	gca	cag	gcc	gag	aag	gag	aag	ctg	ttg		754
Ala	Ile	Arg	Phe	Gly	Arg	Ile	Ala	Gln	Ala	Glu	Lys	Glu	Lys	Leu	Leu		
		180				185					190						
gcg	gag	atc	tcc	agt	gat	atc	gac	cag	ctg	aat	cca	gag	tcc	gct	gac		802
Ala	Glu	Ile	Ser	Ser	Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	Ala	Asp		
195					200					205					210		
ctc	cgt	cag	gcc	ctg	gca	aaa	cat	ttg	tat	gac	tca	tac	ata	aag	tcc		850
Leu	Arg	Gln	Ala	Leu	Ala	Lys	His	Leu	Tyr	Asp	Ser	Tyr	Ile	Lys	Ser		
				215					220					225			
ttc	ccg	ctg	acc	aaa	gca	aag	gcg	agg	gcg	atc	ttg	aca	gga	aag	aca		898
Phe	Pro	Leu	Thr	Lys	Ala	Lys	Ala	Arg	Ala	Ile	Leu	Thr	Gly	Lys	Thr		
			230					235					240				
aca	gac	aaa	tca	cca	ttc	gtt	atc	tat	gac	atg	aat	tcc	tta	atg	atg		946
Thr	Asp	Lys	Ser	Pro	Phe	Val	Ile	Tyr	Asp	Met	Asn	Ser	Leu	Met	Met		
		245					250					255					
gga	gaa	gat	aaa	atc	aag	ttc	aaa	cac	atc	acc	ccc	ctg	cag	gag	cag		994
Gly	Glu	Asp	Lys	Ile	Lys	Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	Glu	Gln		
	260					265					270						
agc	aaa	gag	gtg	gcc	atc	cgc	atc	ttt	cag	ggc	tgc	cag	ttt	cgc	tcc		1042
Ser	Lys	Glu	Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	Arg	Ser		
275					280					285					290		
gtg	gag	gct	gtg	cag	gag	atc	aca	gag	tat	gcc	aaa	agc	att	cct	ggt		1090
Val	Glu	Ala	Val	Gln	Glu	Ile	Thr	Glu	Tyr	Ala	Lys	Ser	Ile	Pro	Gly		
				295					300					305			
ttt	gta	aat	ctt	gac	ttg	aac	gac	caa	gta	act	ctc	ctc	aaa	tat	gga		1138
Phe	Val	Asn	Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	Tyr	Gly		
			310					315					320				
gtc	cac	gag	atc	att	tac	aca	atg	ctg	gcc	tcc	ttg	atg	aat	aaa			

aag agc ctg cga aag cct ttt ggt gac ttt atg gag ccc aag ttt gag	1282
Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu	
355 360 365 370	
ttt gct gtg aag ttc aat gca ctg gaa tta gat gac agc gac ttg gca	1330
Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala	
375 380 385	
ata ttt att gct gtc att att ctc agt gga gac cgc cca ggt ttg ctg	1378
Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu	
390 395 400	
aat gtg aag ccc att gaa gac att caa gac aac ctg cta caa gcc ctg	1426
Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu	
405 410 415	
gag ctc cag ctg aag ctg aac cac cct gag tcc tca cag ctg ttt gcc	1474
Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala	
420 425 430	
aag ctg ctc cag aaa atg aca gac ctc aga cag att gtc acg gaa cac	1522
Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His	
435 440 445 450	
gtg cag cta ctg cag gtg atc aag aag acg gag aca gac atg agt ctt	1570
Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu	
455 460 465	
cac ccg ctc ctg cag gag atc tac aag gac ttg tac tag cagagagtcc	1619
His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr *	
470 475	
tgagccactg ccaacatttc ccttcttcca gttgcactat tctgagggaa aatctgacca	1679
taagaaattt actgtgaaaa agcgtttttaaa aaagaaaagg gtttagaata tgatctattt	1739
tatgcatatt gtttataaag acacattttac aattttacttt taatattaaa aattaccata	1799
ttatgaaatt gc	1811

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<400> 27

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Ile Ser Ser Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe	
20 25 30	
Asp Ile Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro	
35 40 45	
His Tyr Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp	
50 55 60	
Tyr Lys Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val	
65 70 75 80	
Glu Pro Ala Ser Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn	
85 90 95	

006544 011001


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<211> 20
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<213> Homo Sapiens
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20

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<210> 37
<211> 348
<212> DNA
<213> Homo Sapiens
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<211> 246
<212> DNA
<213> Homo Sapiens
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<210>	39
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<213> Homo Sapiens

<223> Xaa = any amino acid

[illegible]

<211> 116

<213> Homo Sapiens

<223> Xaa = any amino acid

[illegible]

115

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 <220>
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 20 25 30
 Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu Ala
 35 40 45
 Trp Arg Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Tyr Ser
 50 55 60
 Ser Thr Ser Arg Pro Ser Ala Pro Pro Thr Thr Ala Thr Ala Phe Asp
 65 70 75 80
 His Leu

<210> 42
 <211> 43
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 <220>
 <223> n = A or T or C or G or other

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 <222> (1)...(43)

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 1 5 10

43

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 <211> 14
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<220>
 <223> Xaa = any amino acid

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 1 5 10

<210> 44
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<223> n = A or T or C or G or other

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1 5 10

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<223> Xaa = any amino acid

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Ser Ala Asn Ile Ser Gln Glu Xaa Ser Glu Tyr Ser Gly Asn
1 5 10

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